L Number	Hits	Search Text	DB	Time stamp
-	1	DmGPCR	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/24 09:38
-	75	drosophila same receptor same coupled	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/24 09:38
-	11	drosophila same receptor same coupled same bind	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/24 09:41

09693746 Results

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RESULT   1
AAU03346
ID   AAU03346 standard; Peptide; 9 AA.
XX
AC   AAU03346;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Fruit fly G protein coupled receptors, DmGPCR6aL/bL ligand #94.
XX
KW   Fruit fly; G protein coupled receptor; DmGPCR6aL/bL;
KW   human immunodeficiency virus; HIV; cancer; Parkinson's disease;
KW   diabetes; obesity; atherosclerosis; thrombosis; stroke; renal
failure;
KW   inflammation; rheumatoid arthritis; autoimmune disorder;
KW   neurological disorder; schizophrenia; manic depression; dementia;
KW   severe mental retardation; dyskinesia; Huntington's disease;
KW   Tourette's syndrome; ligand.
XX
OS   Drosophila melanogaster.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   4
FT                   /note= "Optionally, Tyr has an attached SO3H
moiety"
FT   Modified-site   9
FT                   /note= "C-terminus is amidated"
XX
PN   WO200131005-A2.
XX
PD   03-MAY-2001.
XX
PF   20-OCT-2000; 2000WO-US29002.
XX
PR   22-OCT-1999;   99US-0425676.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Lowery DE,  Smith VG,  Kubiak TA,  Larsen MJ;
XX
DR   WPI; 2001-316333/33.
XX
PT   New Drosophila melanogaster GPCR nucleic acids and polypeptide
useful
PT   for inducing an immune response, for identifying homologs and for
PT   treating e.g. diabetes, obesity and manic depression -
XX
PS   Example 9; Page 101; 110pp; English.
XX
CC   The sequence is a fruit fly G protein coupled receptors,
DmGPCR6aL/bL,
CC   peptide ligand. The proteins are useful for inducing an immune
response
```

CC against itself in a mammal. The nucleic acids are useful for identifying
CC an animal homolog of DmGPCR, by screening databases or libraries. The
CC compounds identified as binding partners or modulators of GPCR binding
CC are useful for treating diseases in animals, and for control insects that
CC are harmful or cause injury to plants or animals. Diseases treated
CC include infections (e.g. viral and human immunodeficiency virus, HIV),
CC cancer, pain, Parkinson's disease, hypotension, hypertension, diabetes,
CC obesity, atherosclerosis, thrombosis, stroke, renal failure,
CC inflammation, rheumatoid arthritis, autoimmune disorders, and psychotic
CC and neurological disorders (anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation, dyskinesias, Huntington's
CC disease or Tourette's syndrome). The nucleic acids can be used for
CC genetic mapping, and producing the GPCRs. Anti-GPCR antibodies can be
CC used in therapy, diagnostic assays and for modulating GPCR activity.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 54; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 FDDYGHLRF 9
|||||||||
Db 1 fddyghlrf 9

RESULT 2
AAU03347
ID AAU03347 standard; Peptide; 9 AA.
XX
AC AAU03347;
XX
DT 12-SEP-2001 (first entry)
XX
DE Fruit fly G protein coupled receptors, DmGPCR6aL/bL ligand #95.
XX
KW Fruit fly; G protein coupled receptor; DmGPCR6aL/bL;
KW human immunodeficiency virus; HIV; cancer; Parkinson's disease;
KW diabetes; obesity; atherosclerosis; thrombosis; stroke; renal failure;
KW inflammation; rheumatoid arthritis; autoimmune disorder;
KW neurological disorder; schizophrenia; manic depression; dementia;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Tourette's syndrome; ligand.

XX
OS Drosophila melanogaster.
XX
FH Key   Location/Qualifiers
FT Modified-site   9
FT   /note= "C-terminus is amidated"
XX
PN WO200131005-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29002.
XX
PR 22-OCT-1999; 99US-0425676.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lowery DE, Smith VG, Kubiak TA, Larsen MJ;
XX
DR WPI; 2001-316333/33.
XX
PT New Drosophila melanogaster GPCR nucleic acids and polypeptide useful
PT for inducing an immune response, for identifying homologs and for
PT treating e.g. diabetes, obesity and manic depression -
XX
PS Example 9; Page 101; 110pp; English.
XX
CC The sequence is a fruit fly G protein coupled receptors, DmGPCR6aL/bL,
CC peptide ligand. The proteins are useful for inducing an immune response
CC against itself in a mammal. The nucleic acids are useful for identifying
CC an animal homolog of DmGPCR, by screening databases or libraries. The
CC compounds identified as binding partners or modulators of GPCR binding
CC are useful for treating diseases in animals, and for control insects that
CC are harmful or cause injury to plants or animals. Diseases treated
CC include infections (e.g. viral and human immunodeficiency virus, HIV),
CC cancer, pain, Parkinson's disease, hypotension, hypertension, diabetes,
CC obesity, atherosclerosis, thrombosis, stroke, renal failure,
CC inflammation, rheumatoid arthritis, autoimmune disorders, and psychotic
CC and neurological disorders (anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation, dyskinesias, Huntington's
CC disease or Tourette's syndrome). The nucleic acids can be used for
CC genetic mapping, and producing the GPCRs. Anti-GPCR antibodies can be
CC used in therapy, diagnostic assays and for modulating GPCR activity.

XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 54; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 FDDYGHLRF 9
||||||||||
Db 1 fddyghlrf 9

RESULT 3
AAU03351
ID AAU03351 standard; Peptide; 9 AA.
XX
AC AAU03351;
XX
DT 12-SEP-2001 (first entry)
XX
DE Fruit fly G protein coupled receptor ligand, drosulfakinin-1.
XX
KW Fruit fly; G protein coupled receptor; drosulfakinin-1;
KW human immunodeficiency virus; HIV; cancer; Parkinson's disease;
KW diabetes; obesity; atherosclerosis; thrombosis; stroke; renal
failure;
KW inflammation; rheumatoid arthritis; autoimmune disorder;
KW neurological disorder; schizophrenia; manic depression; dementia;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Tourette's syndrome; ligand.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Tyr has an attached SO3H moiety"
FT Modified-site 9
FT /note= "C-terminus is amidated"
XX
PN WO200131005-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29002.
XX
PR 22-OCT-1999; 99US-0425676.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lowery DE, Smith VG, Kubiak TA, Larsen MJ;
XX
DR WPI; 2001-316333/33.
XX
PT New Drosophila melanogaster GPCR nucleic acids and polypeptide
useful

PT for inducing an immune response, for identifying homologs and for
PT treating e.g. diabetes, obesity and manic depression -
XX
PS Example 9; Page 98; 110pp; English.
XX
CC The sequence is a fruit fly G protein coupled receptor ligand,
CC drosulfakinin-1. The proteins are useful for inducing an immune
response
CC against itself in a mammal. The nucleic acids are useful for
identifying
CC an animal homolog of DmGPCR, by screening databases or libraries.
The
CC compounds identified as binding partners or modulators of GPCR
binding
CC are useful for treating diseases in animals, and for control
insects that
CC are harmful or cause injury to plants or animals. Diseases treated
CC include infections (e.g. viral and human immunodeficiency virus,
HIV),
CC cancer, pain, Parkinson's disease, hypotension, hypertension,
diabetes,
CC obesity, atherosclerosis, thrombosis, stroke, renal failure,
CC inflammation, rheumatoid arthritis, autoimmune disorders, and
psychotic
CC and neurological disorders (anxiety, schizophrenia, manic
depression,
CC delirium, dementia, severe mental retardation, dyskinesias,
Huntington's
CC disease or Tourette's syndrome). The nucleic acids can be used for
CC genetic mapping, and producing the GPCRs. Anti-GPCR antibodies can
be
CC used in therapy, diagnostic assays and for modulating GPCR
activity.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 54; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

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Qy      1 FDDYGHLRF 9
          |||||||||
Db      1 fddyghlrf 9
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RESULT 4
AAU03353
ID AAU03353 standard; Peptide; 14 AA.
XX
AC AAU03353;
XX
DT 12-SEP-2001 (first entry)
XX
DE Fruit fly G protein coupled receptor ligand, drosulfakinin-2.
XX

KW Fruit fly; G protein coupled receptor; drosulfakinin-2;
KW human immunodeficiency virus; HIV; cancer; Parkinson's disease;
KW diabetes; obesity; atherosclerosis; thrombosis; stroke; renal failure;
KW inflammation; rheumatoid arthritis; autoimmune disorder;
KW neurological disorder; schizophrenia; manic depression; dementia;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Tourette's syndrome; ligand.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /note= "Tyr has an attached SO3H moiety"
FT Modified-site 14
FT /note= "C-terminus is amidated"
XX
PN WO200131005-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29002.
XX
PR 22-OCT-1999; 99US-0425676.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lowery DE, Smith VG, Kubiak TA, Larsen MJ;
XX
DR WPI; 2001-316333/33.
XX
PT New Drosophila melanogaster GPCR nucleic acids and polypeptide useful
PT for inducing an immune response, for identifying homologs and for
PT treating e.g. diabetes, obesity and manic depression -
XX
PS Disclosure; Page 4; 110pp; English.
XX
CC The sequence is a fruit fly G protein coupled receptor ligand,
CC drosulfakinin-2. The proteins are useful for inducing an immune response
CC against itself in a mammal. The nucleic acids are useful for identifying
CC an animal homolog of DmGPCR, by screening databases or libraries. The
CC compounds identified as binding partners or modulators of GPCR binding
CC are useful for treating diseases in animals, and for control insects that
CC are harmful or cause injury to plants or animals. Diseases treated
CC include infections (e.g. viral and human immunodeficiency virus, HIV),
CC cancer, pain, Parkinson's disease, hypotension, hypertension, diabetes,
CC obesity, atherosclerosis, thrombosis, stroke, renal failure,
CC inflammation, rheumatoid arthritis, autoimmune disorders, and psychotic

CC and neurological disorders (anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation, dyskinesias, Huntington's
CC disease or Tourette's syndrome). The nucleic acids can be used for
CC genetic mapping, and producing the GPCRs. Anti-GPCR antibodies can be
CC used in therapy, diagnostic assays and for modulating GPCR activity.
XX
SQ Sequence 14 AA;

Query Match 96.3%; Score 52; DB 22; Length 14;
Best Local Similarity 88.9%; Pred. No. 0.00088;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FDDYGHLRF 9
||||||:||
Db 6 fddyghmrf 14

SEQ ID NO: 22

RESULT 1
AAU03215
ID AAU03215 standard; Protein; 584 AA.
XX
AC AAU03215;
XX
DT 12-SEP-2001 (first entry)
XX
DE Fruit fly G protein coupled receptor, DmGPCR9.
XX
KW Fruit fly; G protein coupled receptor; DmGPCR9;
KW human immunodeficiency virus; HIV; cancer; Parkinson's disease;
KW diabetes; obesity; atherosclerosis; thrombosis; stroke; renal failure;
KW inflammation; rheumatoid arthritis; autoimmune disorder;
KW neurological disorder; schizophrenia; manic depression; dementia;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Tourette's syndrome.
XX
OS Drosophila melanogaster.
XX
PN WO200131005-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29002.
XX
PR 22-OCT-1999; 99US-0425676.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX

PI Lowery DE, Smith VG, Kubiak TA, Larsen MJ;
XX
DR WPI; 2001-316333/33.
DR N-PSDB; AAS05894.
XX
PT New Drosophila melanogaster GPCR nucleic acids and polypeptide useful
PT for inducing an immune response, for identifying homologs and for
PT treating e.g. diabetes, obesity and manic depression -
XX
PS Claim 29; Page 65; 110pp; English.
XX
CC The sequence is a fruit fly G protein coupled receptor, DmGPCR9.
CC The proteins are useful for inducing an immune response against itself in
CC a mammal. The nucleic acids are useful for identifying an animal homolog
CC of DmGPCR, by screening databases or libraries. The compounds identified
CC as binding partners or modulators of GPCR binding are useful for treating
CC diseases in animals, and for control insects that are harmful or cause
CC injury to plants or animals. Diseases treated include infections (e.g.
CC viral and human immunodeficiency virus, HIV), cancer, pain, Parkinson's
CC disease, hypotension, hypertension, diabetes, obesity, atherosclerosis,
CC thrombosis, stroke, renal failure, inflammation, rheumatoid arthritis,
CC autoimmune disorders, and psychotic and neurological disorders (anxiety,
CC schizophrenia, manic depression, delirium, dementia, severe mental
CC retardation, dyskinesias, Huntington's disease or Tourette's syndrome).
CC The nucleic acids can be used for genetic mapping, and producing
CC the GPCRs. Anti-GPCR antibodies can be used in therapy, diagnostic assays
CC and for modulating GPCR activity.
XX
SQ Sequence 584 AA;

Query Match 100.0%; Score 3000; DB 22; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.8e-251;
Matches 584; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

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Qy       1 MFNYEEGDADQAAMAAAAAYRALLDYYANAPSAAGHIVSLNVAPYNGTGNGGTVSLAGNA
60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mfnyeegdadqaamaaaaayralldyyanapsaaghivslnvapyngtgnggtvslagna
60

Qy      61 TSSYGDDDRDGYMDTEPSDLVTELAFSLGTSSSPSPSSTPASSSSTSTGMPVWLIPSYSM
120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 tssygdddrdgymdtepsdlvtelafslgtssspspsstpasssststgmpvwlipsysm
120

Qy     121 ILLFAVLGNLLVISTLVQNRRMRTITNVFLLNLAISDMLLGVLCMPVTLVGTLLRNFIFG
180

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 illfavlgnllvistlvqnrrmrtitnvfllnlaisdmllgvlcmpvtlvgtllrnfifg
180

Qy     181 EFLCKLFQFSQAASVAVSSWTLVAISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGI
240

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 eflcklfqfsqaasvavsswtlvaisceryyaichplrsrswqtishaykiigfiwlggi
240

Qy     241 LCMTPIAVFSQLIPTSRPGYCKCREFWPDQGYELFYNILLDFLLLVLPLLVLCVAYILIT
300

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 lcmtpiavfsqliptsrpgyckcrefwpdqgyelfynilldflllvlpllvlcvayilit
300

Qy     301 RTLYVGMAKDSGRILQQSLPVSATTAGGSAPNPGTSSSSNCILVLTATAVYNENSNNNNG
360

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 rtlyvgmakdsgrilqqslpvsattaggsapnpgtssssncilvltatavynensnnnng
360

Qy     361 NSEGSAGGGSTNMATTTLTTRPTAPTVITTTTTTTVTLAKTSSPSIRVHDAALRRSNEAK
420

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 nsegsagggstnmatttlttrptaptvitttttttvtlaktsspsirvhdaalrrsneak
420

Qy     421 TLESKKRVVKMLFVLVLEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSS
480

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 tleskkrvvkmlfvlvlefficwtplyvintmvmligpvvyeyvdytaisflqllaysss
480

Qy     481 CCNPITYCFMNASFRRAFVDTFKGLPWRRGAGASGGVGGAAGGGLSASQAGAGPGAYASA
540

                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ccnpitycfmnasfrrafvdtfkglpwrrgagasggvggaaggglsasqagagpgayasa
540

Qy     541 NTNISLNPGLAMGMGTWRSRSRHEFLNAVVTTNSAAAAVNSPQL 584
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Db     541 ntnislnpglamgmgtwrsrsrheflnavvttnsaaaavnspql 584
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PYRB_LACLA
ID   PYRB_LACLA     STANDARD;      PRT;   310 AA.
AC   Q9CF79;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
DE   transcarbamylase) (ATCase).
GN   PYRB OR LL1602.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC   Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
CC   -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
CC       + N-carbamoyl-L-aspartate.
CC   -!- PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.
CC   -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE006390; AAK05700.1; -.
DR   InterPro; IPR002029; Carbmyltransf_asor.
DR   Pfam; PF00185; OTCace; 1.
DR   Pfam; PF02729; OTCace_N; 1.
DR   PRINTS; PR00100; AOTCASE.
DR   PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
KW   Pyrimidine biosynthesis; Transferase; Complete proteome.
SQ   SEQUENCE   310 AA;  34558 MW;  EEDE6B8EC6F00B94 CRC64;


  Query Match             72.2%;  Score 39;  DB 1;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 5;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FDDYGH 6
           ||||||
Db     201 FDDYGH 206


RESULT  12
RL5_SULSO
ID   RL5_SULSO      STANDARD;      PRT;   182 AA.
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AC   Q9UX93;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   50S ribosomal protein L5P.
GN   RPL5P OR RPL5AB OR SSO0704 OR C10_026.
OS   Sulfolobus solfataricus.
OC   Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX   NCBI_TaxID=2287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35092 / DSM 1617 / P2;
RX   MEDLINE=20165948; PubMed=10701121;
RA   Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
RA   Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
RA   Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
RA   Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
RA   St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
RA   Ragan M.A., Sensen C.W.;
RT   "Gene content and organization of a 281-kbp contig from the genome of
RT   the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
RL   Genome 43:116-136(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35092 / DSM 1617 / P2;
RX   MEDLINE=21332296; PubMed=11427726;
RA   She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA   Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA   De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA   Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA   Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA   Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA   Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT   "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
CC   -!- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y18930; CAB57599.1; -.
DR   EMBL; AE006696; AAK41006.1; -.
DR   InterPro; IPR002132; Ribosomal_L5.
DR   Pfam; PF00281; Ribosomal_L5; 1.
DR   Pfam; PF00673; Ribosomal_L5_C; 1.
DR   ProDom; PD001076; Ribosomal_L5; 1.
DR   PROSITE; PS00358; RIBOSOMAL_L5; FALSE_NEG.
KW   Ribosomal protein; Complete proteome.
SQ   SEQUENCE   182 AA;  20652 MW;  3070C4B01860D448 CRC64;
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Query Match 70.4%; Score 38; DB 1; Length 182;

Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 6; Conservative 2; Mismatc

09693746 Results

SEQ ID NO: 22

SUMMARIES

Result No	Score	% Query Match	Length	DB	ID	Description
1	3000	100.0	584	22	AAU03215	Fruit fly G protei
2	1708	56.9	415	22	ABB62762	Drosophila melanog
3	1708	56.9	415	22	AAU38944	Drosophila G-prote
4	1704	56.8	407	22	AAB86963	D. melanogaster pe
5	1242	41.4	749	22	ABB62718	Drosophila melanog
6	1242	41.4	749	22	AAU38943	Drosophila G-prote
7	970	32.3	201	22	AAB86962	D. melanogaster pe
8	964	32.1	205	22	ABB62772	Drosophila melanog
9	655.5	21.9	451	14	AAR40771	Sequence encoded b
10	655.5	21.9	452	22	AAB66619	Rat brain CCKB rec
11	654.5	21.8	430	14	AAR40772	Sequence encoded b
12	654.5	21.8	430	22	AAB66625	Guinea pig CCKA re
13	654.5	21.8	450	22	AAB66626	Guinea pig CCKA re
14	652.5	21.8	450	15	AAR53263	M. matalensis CCK
15	652.5	21.8	450	15	AAR59290	Mastomys gastrin r
16	647.5	21.6	428	18	AAW29102	Human peptide horm
17	647.5	21.6	428	22	AAB66630	Human CCK A recept
18	642	21.4	444	14	AAR38890	Sequence encoded b

RESULT 9
AAR40771
ID AAR40771 standard; protein; 451 AA.
XX
AC AAR40771;
XX
DT 07-FEB-1994 (first entry)
XX
DE Sequence encoded by the rat brain cholecystokinin (CCK) B
DE receptor cDNA clone.
XX
KW Cholecystokinin receptor protein; CCK; gastrointestinal receptor.
XX
OS Balaenoptera acutorostrata.
XX

FH	Key	Location/Qualifiers
FT	Modified-site	6
FT		/label= glycosylation site
FT		/note= "see also AAs 30,36,255"
FT	Domain	57..80
FT		/label= transmembrane I
FT	Domain	93..116
FT		/label= transmembrane II
FT	Domain	131..150
FT		/label= transmembrane III
FT	Domain	173..192
FT		/label= transmembrane IV
FT	Domain	219..242
FT		/label= transmembrane V
FT	Domain	339..359
FT		/label= transmembrane VI
FT	Domain	374..381
FT		/label= transmembrane VII

XX
PN WO9316182-A.
XX
PD 19-AUG-1993.
XX
PF 28-JAN-1993; 93WO-US00466.
XX

PR 07-FEB-1992; 92US-0831248.
PR 01-APR-1992; 92US-0861769.
PR 11-AUG-1992; 92US-0928033.
PR 02-SEP-1992; 92US-0937609.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Wank SA;
XX
DR WPI; 1993-272886/34.
DR N-PSDB; AAQ47668.
XX
PT Isolated DNA molecule encoding cholecystokinin receptor protein -
PT are purified to isolate cholecystokinin receptor clones and
PT produce anti-cholecystokinin receptor antibodies
XX
PS Claim 19; Figure 2; 110pp; English.
XX
CC The rat brain CCK B receptor cDNA clone encodes a protein with
CC 7 transmembrane domains, and homology with CCK A type receptor and
CC other G-protein receptor superfamily members. There are 4 potential
CC sites of N-linked glycosylation, for serine phosphorylation
CC (82,154,441), for disulphide bridges (127,205) and palmitoylation
CC (413).
XX
SQ Sequence 451 AA;

Query Match 21.9%; Score 655.5; DB 14; Length 451;
Best Local Similarity 38.6%; Pred. No. 2.6e-48;
Matches 164; Conservative 62; Mismatches 144; Indels 55; Gaps 11;

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Qy      88 LGTSSSPSPSSTPASSSSTST---GMPVWLIPSYSMILLFAVLGNLLVISTLVQNRRMRT 144
           | :||: : |  |      | |    | :  |  |::| | :| ||:|:|  |  :||:||
Db      29 lnsssagnlscdpprirgtgtrelemai-ritlyaviflmsvggnvliivvlglsrrlrt 87

Qy     145 ITNVFLLNLAISDMLLGVLCMPVTLVGTLLRNFIFGEFLCKLFQFSQAASVAVSSWTLVA 204
           :|| |||:||:||:|| | ||| ||:  |:  ||||  :||    .    ||:||:  |||
Db      88 vtnafllslavsdlllavacmpftllpnlmgtfifgtvickaisylmgvsvsvstlnlva 147

Qy     205 ISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIAVFSQLIPTSRPGYCKCR 264
           |: ||| ||| ||::| ||| ||| ::|   ||   | | |  |:: : |   |   :|
Db     148 ialerysaicrplqarvwqtrshaarvilatwllsgllmvpypvytmvqpvg-prvlqcm 206

Qy     265 EFWPDQGYELFYNILLDFLLLVLPLLVLCVAYILITRTLYVGMAKD--------SGRILQ 316
             ||    :  :::||  ||  :| :|: ||| ||:| ||:|:  |         |    |
Db     207 hrwpsarvqqtwsvlllllffipgvviavayglisrelylglhfdgendsetqsrarnq 266

Qy     317 QSLPVSATTAGGSAPNPGTSSSSNCILVLTATAVYNENSNNNNGNSEGSAGGGSTNMATT 376
             ||       ||:|| |    :  |  |   |:|  |:|:           |    :  :
Db     267 gglp------ggaapgp-vhqnggcrpv---tsvagedsd----------gccvqlprs 305

Qy     377 TLTTRPTAPTVITTTTTTTVTLAKTSSPSIRVHDAALRRSNEAKTLESKKRVVKMLFVLV 436
           |            || || |      |          | |:|| | :|||||:|| |:|
Db     306 rl----------emttlttptpgpvpgp----------rpnqakll-akkrvvrmllviv 344

Qy     437 LEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSSCCNPITYCFMNASFRR 496
           | ||:|| |:| :||     ||     :    |||: ||:| |:| ||: ||||:  ||:
Db     345 llfflcwlpvysvntwrafdgpgaqralsgapisfihllsyvsacvnplvycfmhrrfrq 404

Qy     497 AFVDT 501
           | :||
Db     405 acldt 409
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Issued:

Result No.	Score	Query Match	Length	DB	ID	Description

1	664.5	22.1	453	1	US-08-570-157-7	Sequence 7, Appli
2	656	21.9	451	1	US-08-570-157-2	Sequence 2, Appli
3	655.5	21.9	452	1	US-07-937-609-16	Sequence 16, Appl
4	655.5	21.9	452	4	US-08-029-170-16	Sequence 16, Appl
5	654.5	21.8	430	1	US-07-937-609-23	Sequence 23, Appl
6	654.5	21.8	430	2	US-08-919-624-3	Sequence 3, Appli
7	654.5	21.8	430	4	US-08-029-170-23	Sequence 23, Appl
8	654.5	21.8	450	1	US-07-937-609-24	Sequence 24, Appl
9	654.5	21.8	450	4	US-08-029-170-24	Sequence 24, Appl
10	648.5	21.6	449	1	US-08-570-157-1	Sequence 1, Appli
11	647.5	21.6	428	1	US-08-570-157-5	Sequence 5, Appli
12	647.5	21.6	428	4	US-08-029-170-31	Sequence 31, Appl
13	642	21.4	444	1	US-07-937-609-14	Sequence 14, Appl
14	642	21.4	444	4	US-08-029-170-14	Sequence 14, Appl
15	632.5	21.1	443	1	US-08-570-157-6	Sequence 6, Appli
16	626.5	20.9	453	1	US-07-937-609-26	Sequence 26, Appl
17	626.5	20.9	453	4	US-08-029-170-26	Sequence 26, Appl
18	624	20.8	448	1	US-08-570-157-3	Sequence 3, Appli
19	619.5	20.6	447	1	US-07-937-609-29	Sequence 29, Appl
20	619.5	20.6	447	4	US-08-029-170-29	Sequence 29, Appl
21	619.5	20.6	453	1	US-07-937-609-27	Sequence 27, Appl
22	619.5	20.6	453	1	US-07-978-892A-5	Sequence 5, Appli
23	619.5	20.6	453	1	US-08-570-157-4	Sequence 4, Appli
24	619.5	20.6	453	4	US-08-029-170-27	Sequence 27, Appl
25	617.5	20.6	447	1	US-07-978-892A-6	Sequence 6, Appli
26	442	14.7	432	4	US-09-255-368-2	Sequence 2, Appli
27	420.5	14.0	430	4	US-09-255-368-8	Sequence 8, Appli
28	415.5	13.8	444	4	US-09-119-788-2	Sequence 2, Appli
29	401	13.4	425	4	US-09-479-128-2	Sequence 2, Appli
30	400	13.3	402	3	US-08-846-704-4	Sequence 4, Appli
31	399	13.3	420	4	US-09-255-368-6	Sequence 6, Appli

RESULT 1
US-08-570-157-7
; Sequence 7, Application US/08570157
; Patent No. 5750353
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
; TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,157
; FILING DATE: 11-DEC-1995
; CLASSIFICATION 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER 00398/109001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

, LENGTH: 453 amino acids
, TYPE: amino acid
, STRANDEDNESS not relevant
, TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-570-157-7

Query Match 22.1%; Score 664.5; DB 1; Length 453;
Best Local Similarity 33.5%; Pred. No. 2.9e-45;
Matches 176; Conservative 77; Mismatches 170; Indels 103; Gaps 16;

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Qy     13 AMAAAAAAYRALLDYYANAPSAAGHIVSLNVAPYNGTGNGGTVSLAG---NATSSYGDDDR 69
          :::  :|   ||  |:|        ::  ::  ||| |  | :      | |       ||
Db      6 SLSNISALHELLCRYSNLSGT----LTWNLSSTNGTHNLTTANWPPWNLNCTPIL---DR 58

Qy     70 DGYMDTEPSDLVTELAFSLGTSSSPSPSSTPASSSSTSTGMPVWL-IPSYSMILLFAVLG 128
                                  ||||            : :|: |  ||:|   :| |
Db     59 ----------------------KKPSPSD----------LNLWVRIVMYSVIFLLSVFG 85

Qy    129 NLLVISTLVQNRRMRTITNVFLLNLAISDMLLGVLCMPVTLVGTLLRNFIFGEFLCKLFQ 188
          |  :|  ||  :|:|||   |||:||:| ::: ||||| ||:  |: ||||||  :|:
Db     86 NTLIIIVLVMNKRLRTITNSFLLSLALSDLMVAVLCMPFTLIPNLMENFIFGEVICRAAA 145

Qy    189 FSQAASVAVSSWTLVAISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIAV 248
          :   ||:| :: ||||  ||| |||:|  || ||| ||||::|   |:   : ; |  |
Db    146 YFMGLSVSVSTFNLVAISIERYSAICNPLXSRVWQTRSHAYRVIAATWVLSSIIMIPYLV 205

Qy    249 FSQLI----PTSRPGYCKCREFWPDQGYELFYNILLDFLLLVLPLLVLCVAYILITRTLY 304
          ::: :       | |: :||  ||  :  : :||  :|  :| :|: ||| |':| ||
Db    206 YNKTVTFPMKDRRVGH-QCRLVWPSKQVQQAWYVLLLTILFFIPGVVMIVAYGLISRELY 264

Qy    305 VGMAKDSGRILQQSLPVSATTAGGSAPN--PGTSSSSNCILVLTATAVYNENSNNNNGNS 362
          |:  :   :  :   |  | | |   |       | : :|
Db    265 RGIQFE----MDLNKEAKAHKNGVSTPTTIPSGDEGDGCYIQVTKR---------- 306

Qy    363 EGSAGGGSTNMATTTLTTRPTAPTVITTTTTTTVTLAKTSSPSIRVHDAALRRSNEAKTL 422
                 :|||     |:| |                    | |   ::||| .
Db    307 -------RNTMEMSTLT-----PSVCTKM----------DRARINNSEAK-L 335

Qy    423 ESKKRVVKMLFVLVLEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSSCC 482
          :|||::|| |:|  ;|||| |::. ||         :  :    |||: ||:|:|:|
Db    336 MAKKRVIRMLIVIVAMFFICWMPIFVANTWKAFDELSAFNTLTGAPISFIHLLSYTSACV 395

Qy    483 NPITYCFMNASFRRAFVDTFKGL--PWRRGAGASGGVGGAAGGGLS 526
          :|  |||||  ||:||: ||       |        :  | |  ||
Db    396 NPLIYCFMNKRFRKAFLGTFSSCIKPCRNFRDTDEDI-AATGASLS 440
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655.5	21.9	452	2	A46195	cholecystokinin B
2	654.5	21.8	430	2	I51898	cholecystokinin A
3	652.5	21.8	450	2	JQ1614	gastrin receptor -
4	647.5	21.6	428	2	JN0692	cholecystokinin ty
5	644.5	21.5	436	2	JC5599	cholecystokinin-A
6	642	21.4	444	2	A42685	cholecystokinin re
7	629.5	21.0	427	2	S50150	gastric CCK-A rece
8	625	20.8	452	2	JC2459	gastrin/cholecysto
9	619.5	20.6	453	2	S32817	gastrin receptor -
10	617.5	20.6	447	2	A47430	gastrin/cholecysto
11	459.5	15.3	381	2	S48049	cholecystokinin B
12	427.5	14.2	397	2	T25910	hypothetical prote
13	420.5	14.0	449	2	A41738	neuropeptide Y rec
14	382.5	12.8	465	1	JQ1517	neurokinin 3 recep
15	372.5	12.4	452	2	A34916	neurokinin 3 recep
16	370.5	12.3	407	2	S23510	neurokinin 1 recep
17	367.5	12.2	440	2	A44081	kappa-type opioid

18 366 12.2 385 2 S55524 neurokinin 3 recep

RESULT 1
A46195
cholecystokinin B receptor subtype - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: A46195
R;Wank, S.A.; Pisegna, J.R.; de Weerth, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992
A;Title: Brain and gastrointestinal cholecystokinin receptor family structure and functional expression
A;Reference number: A46195; MUID:92409582
A;Accession: A46195
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-452 <WAN>
A;Cross-references: GB:M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBIP:114084)
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.9%; Score 655.5; DB 2; Length 452;
Best Local Similarity 38.6%; Pred. No. 2.5e-38;
Matches 164; Conservative 62; Mismatches 144; Indels 55; Gaps 11;

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Qy      88 LGTSSSPSPSSTPASSSSTST---GMPVWLIPSYSMILLFAVLGNLLVISTLVQNRRMRT 144
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Db      29 LNSSSAGNLSCDPPRIRGTGTRELEMAI-RITLYAVIFLMSVGGNVLIIVVLGLSRRLRT 87

Qy     145 ITNVFLLNLAISDMLLGVLCMPVTLVGTLLRNFIFGEFLCKLFQFSQAASVAVSSWTLVA 204
           :|: |||: |  |:|| | ||| ||:  |:  |||  :|.   :    ||:||.  |||
Db      88 VTNAFLLSLAVSDLLLAVACMPFTLLPNLMGTFIFGTVICKAISYLMGVSVSVSTLNLVA 147

Qy     205 ISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIAVFSQLIPTSRPGYCKCR 264
           |: ||| |:| ;|::| ||| ||| ::|    |   | |    |:: : |   |   :|
Db     148 IALERYSAICRPLQARVWQTRSHAARVILATWLLSGLLMVPYPVYTMVQPVG-PRVLQCM 206

Qy     265 EFWPDQGYELFYNILLDFLLLVLPLLVLCVAYILITRTLYVGMAKD--------SGRILQ 316
             ||    .   ::||  ||  :| :|: ||  ||:| ||. :  |            |
Db     207 HRWPSARVQQTWSVLLLLLLFFIPGVVIAVAYGLISRELYLGLHFDGENDSETQSRARNQ 266

Qy     317 QSLPVSATTAGGSAPNPGTSSSSNCILVLTATAVYNENSNNNNGNSEGSAGGGSTNMATT 376
           ||      ||:'| |    :  |  |   |:|  |:|:          |    :  :
Db     267 GGLP------GGAAPGP-VHQNGGCRPV---TSVAGEDSD----------GCCVQLPRS 305

Qy     377 TLTTRPTAPTVITTTTTTTVTLAKTSSPSIRVHDAALRRSNEAKTLESKKRVVKMLFVLV 436
           |           || || |       |          | .:|| | :|||||: | |:|
Db     306 RL----------EMTTLTTPTPGPVPGP----------RPNQAKLL-AKKRVVRMLLVIV 344

Qy     437 LEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSSCCNPITYCFMNASFRR 496
           | ||:|| |:| : |     ||     :    |||: ||:  |:| ||: ||||.  ||:
Db     345 LLFFLCWLPVYSVNTWPAFDGPGAQRALSGAPISFIHLLSYVSACVNPLVYCFMHRRFRQ 404

Qy     497 AFVDT 501
           | :||
Db     405 ACLDT 409
```

RESULT 2
I51898
cholecystokinin A receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Apr-2000
C;Accession: I51898
R;De Weerth, A.; Pisegna, J.R.; Wank, S.A.
Am. J. Physiol. 265, G1116-G1121, 1993

A;Title: Guinea pig gallbladder and pancreas possess identical CCK-A receptor subtypes: receptor cloning and expression.
A;Reference number: I51898, MUID:94106629
A;Accession: I51898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-430 <RES>
A;Cross-references: GB:S68242; NID:g544723; PIDN:AAB29504.1, PID g544724
C;Superfamily: neurokinin 1 receptor

Query Match 21.8%; Score 654.5; DB 2; Length 430;
Best Local Similarity 35.0%; Pred. No. 2.7e-38;
Matches 165; Conservative 72; Mismatches 168; Indels 67, Gaps 10;

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Qy      83 ELAF---SLGTSSSPSPSSTPASSSSTSTGMPVWLIPSYSMILLFAVLGNLLVISTLVQN 139
           :| :   :|      | .|              |   |  || |   :||| |||   : |
Db      19 ELGFENETLFCLDRPRPS---------KEWQPAVQILLYSLIFLLSVLGNTLVITVLIRN 69

Qy     140 RRMRTITNVFLLNLAISDMLLGVLCMPVTLVGTLLRNFIFGEFLCKLFQFSQAASVAVSS 199
           .||||:| :|||.||: |.:| : ||   |: :||::|||  .||   .  .| | :
Db      70 KRMRTVTNIFLLSLAVSDLMLCLFCMPFNLIPSLLKDFIFGSAVCKTTTYFMGTSVSVST 129

Qy     200 WTLVAISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIAVFSQLIPTSRPG 259
           . ||||| ||: ||| |.|| ||| :|| |:|          .||  ::| |:  ::
Db     130 FNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFTIMTPYPIYSNLVPFTKNN 189

Qy     260 Y---CKCREFWPDQGYELFYNILLDFLLLVLPLLVLCVAYILITRTLYVGMAKDSGRILQ 316
               |:   |.   :  ::  |  :| ::| :|: ||| ||  || :  |:  | :
Db     190 NQTGNMCRFLLPNDVMQQTWHTFLLLILFLIPGIVMMVAYGLISLELYQGIKFDA--IQK 247

Qy     317 QSLPVSATTAGGSAPNPGTSSSSNCILVLTATAVYNENSNNNNGNSEGSAGGGSTNMATT 376
           :|      |: |   |       |  |          | . | :
Db     248 KSAKERKTSTGSSGP---MEDSDGC---------YLQKSRH----------PR 278

Qy     377 TLTTRPTAPTVITTTTTTTVTLAKTSSPSIRVHDAALRRSNEAKTLESKKRVVKMLFVLV 436
           |  |  :|                 : | : |::   :| |.     | :||| :: | | |
Db     279 KLELRQLSP---------------SSSGSNRIN--RIRSSSSTANLMAKKRVIRMLIVIV 321

Qy     437 LEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSSCCNPITYCFMNASFRR 496
           :  |:|| .::  |            ::  | |||: ||: :|'| ||| |: ||  |
Db     322 VLFFLCWMPIFSANAWRAYDTVSAERHLSGTPISFILLLSYTSSCVNPIIYCFMNKRFRL 381

Qy     497 AFVDTFKGLPWRRGAGASGGVGGAAGGGLSASQAGAGPGAYASANTNISLNP 548
           |: ||          : || |  :        ||     :  : : |  |
Db     382 GFMATFPCCP----NPGTPGVRGEMGEEEEGRTTGASLSRYSYSHMSTSAPP 429
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	667.5	22.2	453	1	CCKR_XENLA	P70031 xenopus lae
2	655.5	21.9	452	1	GASR_RAT	P30553 rattus norv
3	654.5	21.8	430	1	CCKR_CAVPO	Q63931 cavia porce
4	652.5	21.8	450	1	GASR_PRANA	P30796 praomys nat
5	647.5	21.6	428	1	CCKR_HUMAN	P32238 homo sapien
6	646.5	21.6	453	1	GASR_MOUSE	P56481 mus musculu
7	644.5	21.5	436	1	CCKR_MOUSE	O08786 mus musculu
8	642	21.4	444	1	CCKR_RAT	P30551 rattus norv
9	632.5	21.1	427	1	CCKR_RABIT	O97772 oryctolagus
10	625	20.8	452	1	GASR_RABIT	P46627 oryctolagus
11	619.5	20.6	453	1	GASR_CANFA	P30552 canis famil
12	617.5	20.6	447	1	GASR_HUMAN	P32239 homo sapien
13	612	20.4	454	1	GASR_BOVIN	P79266 bos taurus
14	442	14.7	432	1	NFF1_RAT	Q9ep86 rattus norv

```
RESULT   1
CCKR_XENLA
ID   CCKR_XENLA     STANDARD;      PRT;   453 AA.
AC   P70031;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Cholecystokinin receptor (CCK-XLR).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96319796; PubMed=8700154;
RA   Schmitz F., Pratt D S., Wu M.-J., Kolakowski L F. Jr., Beinborn M.,
RA   Kopin A.S.;
RT   "Identification of cholecystokinin-B/gastrin receptor domains that
RT   confer high gastrin affinity: utilization of a novel Xenopus laevis
RT   cholecystokinin receptor.";
RL   Mol. Pharmacol. 50:436-441(1996).
CC   -!- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. THIS RECEPTOR MEDIATES ITS
CC       ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A
CC       PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. HAS HIGH
CC       AFFINITY FOR CCK-8 AND LOW AFFINITIES FOR GASTRIN-17-I, CCK-4, AND
CC       UNSULFATED CCK-8.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: BRAIN AND STOMACH.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       HAS EQUAL SIMILARITY TO TYPE A AND B CHOLECYSTOKININ MAMMALIAN
CC       RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U49258; AAB09052.1; -.
DR   GCRDb; GCR_0930; -.
DR   GCRDb; GCR_1953; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Lipoprotein; Palmitate.
FT   DOMAIN        1     64       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     65     94       1 (POTENTIAL).
FT   DOMAIN       95    104       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    105    131       2 (POTENTIAL)
FT   DOMAIN      132    142       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    143    164       3 (POTENTIAL).
FT   DOMAIN      165    184       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    185    205       4 (POTENTIAL).
FT   DOMAIN      206    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    261       5 (POTENTIAL).
FT   DOMAIN      262    343       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    344    364       6 (POTENTIAL).
FT   DOMAIN      365    379       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    380    403       7 (POTENTIAL).
FT   DOMAIN      404    453       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    141    223       BY SIMILARITY
FT   LIPID       401    401       PALMITATE (BY SIMILARITY).
FT   CARBOHYD      9      9       N-LINKED (GLCNAC  . .) (POTENTIAL).
FT   CARBOHYD     22     22       N-LINKED (GLCNAC  . .) (POTENTIAL).
```

```
FT   CARBOHYD      30      30       N-LINKED (GLCNAC.    .) (POTENTIAL).
FT   CARBOHYD      35      35       N-LINKED (GLCNAC.    .) (POTENTIAL).
FT   CARBOHYD      39      39       N-LINKED (GLCNAC.    .) (POTENTIAL).
SQ   SEQUENCE   453 AA;  51157 MW;  06217927B7482678 CRC64;


  Query Match             22.2%;  Score 667.5;  DB 1;  Length 453;
  Best Local Similarity   33.5%;  Pred. No. 6.4e-34;
  Matches  176;  Conservative   78;  Mismatches  169;  Indels  103;  Gaps   16;

Qy      13 AMAAAAAAYRALLDYYANAPSAAGHIVSLNVAPYNGTGNGGTVSLAG---NATSSYGDDDR 69
           :::  :|   ||  |:|         ::  :   ||| |  |           |      |
Db       6 SLSNISALHELLCRYSNLSGT----LTWNLSSTNGTHNLTTANWPPWNLNCTPIL---DR 58

Qy      70 DGYMDTEPSDLVTELAFSLGTSSSPSPSSTPASSSSTSTGMPVWL-IPSYSMILLFAVLG 128
                                  :|||           : .|: |   |:  . :| |
Db      59 ---------- ------------KKPSPSD----------LNLWVRIVMYSVIFLLSVFG 85

Qy     129 NLLVISTLVQNRRMRTITNVFLLNLAISDMLLGVLCMPVTLVGTLLRNFIFGEFLCKLFQ 188
           |:|   |  :|:|_||  |:|:|:|:     ||||| : :  |: | ||  .|:
Db      86 NTLIIIVLVMNKRLRTITNSFLLSLALSDLMVAVLCMPFTLIPNLMENFIFGEVICRAAA 145

Qy     189 FSQAASVAVSSWTLVAISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIAV 248
           :   ||:| :: ||_:|| ||  : |:|  . : |:| |_| ::|    :   : : |  |
Db     146 YFMGLSVSVSTFNLVAISIERYSAICNPLKSRVWQTRSHAYRVIAATWVLSSIIMIPYLV 205

Qy     249 FSQLI----PTSRPGYCKCREFWPDQGYELFYNILLDFLLLVLPLLVLCVAYILITRTLY 304
           :: :       | |: :||  || :  . . :||  :|  :| :|. .|: | :| |
Db     206 YNKTVTFPMKDRRVGH-QCRLVWPSKQVQQAWYVLLLTILFFIPGVVMIVAYGLISRELY 264

Qy     305 VGMAKDSGRILQQSLPVSATTAGGSAPN--PGTSSSSNCILVLTATAVYNENSNNNNGNS 362
           |:  :    :  :    |   | | |          | : :|
Db     265 RGIQFE----MDLNKEAKAHKNGVSTPTTIPSGDEGDGCYIQVTKR-------------- 306

Qy     363 EGSAGGGSTNMATTTLTTRPTAPTVITTTTTTTVTLAKTSSPSIRVHDAALRRSNEAKTL 422
                     :|||     |:| |                    | |   ::||| |
Db     307 --------RNTMEMSTLT-----PSVCTKM----------------DRARINNSEAK-L 335

Qy     423 ESKKRVVKMLFVLVLEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSSCC 482
           :|:||::|  |:|  ||||  |::| |          :  :    |||: ||: :|:!
Db     336 MAKKRVIRMLIVIVAMFFICWMPIFVANTWKAFDELSAFNTLTGAPISFIHLLSYTSACV 395

Qy     483 NPITYCFMNASFRRAFVDTFKGL--PWRRGAGASGGVGGAAGGGLS 526
           ||: |||  |  ||:| : ||     | |       :  | |  ||
Db     396 NPLIYCFMNKRFRKAFLGTFSSCIKPCRNFRDTDEDI-AATGASLS 440


SEQ ID NO: 157


%
Result          Query
  No.   Score  Match Length DB  ID                      Description
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     1      54  100.0      9  22  AAU03346                Fruit fly G protei
     2      54  100.0      9  22  AAU03347                Fruit fly G protei
     3      54  100.0      9  22  AAU03351                Fruit fly G protei
     4      52   96.3     14  22  AAU03353                Fruit fly G protei
     5      52   96.3    128  22  ABB66665                Drosophila melanog
     6      48   88.9      9  22  AAU03897                G protein-coupled
     7      40   74.1      7  22  AAU03354                G protein coupled
     8      40   74.1    590  22  AAB84261                Amino acid sequenc
     9      40   74.1    640  22  ABG16509                Novel human diagno
    10      40   74.1    836  19  AAW85017                Grk5-green floures
    11      40   74.1    842  19  AAW85008                Grk5-green floures
    12      39   72.2    227  22  AAU31534                Novel human secret
    13      39   72.2    255  22  ABB71872                Drosophila melanog
    14      39   72.2    345  22  AAU33607                Pseudomonas aerugi
    15      38   70.4    281  22  ABB59929                Drosophila melanog
    16      37   68.5     89  22  AAM16451                Peptide #2885 enco
```

17	37	68.5	145	22	AAM25650	Human protein sequ
18	37	68.5	431	20	AAY59728	Human normal ovari
19	37	68.5	855	21	AAB54359	Human pancreatic c
20	37	68.5	1090	22	AAB94737	Human protein sequ
21	37	68.5	1144	21	AAB02007	Type III adenylyl
22	36	66.7	149	22	AAM79774	Human protein SEQ
23	36	66.7	244	21	AAG07361	Arabidopsis thalia
24	36	66.7	244	21	AAG61263	Arabidopsis thalia
25	36	66.7	251	21	AAG07360	Arabidopsis thalia
26	36	66.7	251	21	AAG61262	Arabidopsis thalia
27	36	66.7	253	22	AAB86351	A. thaliana allene
28	36	66.7	254	22	AAB86350	A. thaliana allene
29	36	66.7	258	21	AAG07359	Arabidopsis thalia
30	36	66.7	258	21	AAG61261	Arabidopsis thalia
31	36	66.7	301	22	AAM78790	Human protein SEQ

SUMMARIES

Result No	Score	% Query Match	Length	DB	ID	Description
1	40	74.1	590	1	US-08-221-817-14	Sequence 14, Appl
2	40	74.1	590	1	US-08-454-439-14	Sequence 14, Appl
3	40	74.1	590	4	US-08-464-954A-5	Sequence 5, Appli
4	40	74.1	590	5	PCT-US94-10487-14	Sequence 14, Appl
5	37	68.5	1144	3	US-08-726-214-6	Sequence 6, Appli
6	35	64.8	576	1	US-08-221-817-13	Sequence 13, Appl
7	35	64.8	576	1	US-08-221-817-22	Sequence 22, Appl
8	35	64.8	576	1	US-08-454-439-13	Sequence 13, Appl
9	35	64.8	576	1	US-08-454-439-22	Sequence 22, Appl
10	35	64.8	576	4	US-08-464-954A-6	Sequence 6, Appli
11	35	64.8	576	5	PCT-US94-10487-13	Sequence 13, Appl
12	35	64.8	576	5	PCT-US94-10487-22	Sequence 22, Appl
13	35	64.8	632	1	US-08-221-817-11	Sequence 11, Appl
14	35	64.8	632	1	US-08-454-439-11	Sequence 11, Appl
15	35	64.8	632	5	PCT-US94-10487-11	Sequence 11, Appl
16	35	64.8	688	1	US-08-221-817-19	Sequence 19, Appl
17	35	64.8	688	1	US-08-454-439-19	Sequence 19,

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RESULT   1
US-08-221-817-14
; Sequence 14, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
,    TITLE OF INVENTION:  Kinase GRK6
,    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
,      CITY:  Chicago
,      STATE:  Illinois
,      COUNTRY:  USA
,      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
,      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
,    CURRENT APPLICATION DATA:
,      APPLICATION NUMBER   US/08/221,817
,      FILING DATE
,      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER   08/123,932
```

FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 553215land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION
TELEPHONE (312) 474-6300
TELEFAX (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
TYPE: amino acid
TOPOLOGY linear
MOLECULE TYPE: protein
US-08-221-817-14

Query Match 74.1%; Score 40; DB 1; Length 590;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6, Conservative 1, Mismatches 0; Indels 0; Gaps 0;

Qy 2 DDYGHLR 8
| ||| :
Db 320 DDYGHIR 326

RESULT 2
US-08-454-439-14
; Sequence 14, Application US/08454439
; Patent No. 5591618
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION. A No. 5591618el G Protein-Coupled Receptor
; TITLE OF INVENTION Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE. Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,439
; FILING DATE: 30-MAY-1995
; CLASSIFICATION 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/221,817
; FILING DATE 31-MAR-1994
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5591618and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELECOMMUNICATION INFORMATION.
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX 25-3856
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

; LENGTH 590 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-454-439-14

Query Match 74.1%; Score 40; DB 1; Length 590;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 DDYGHLR 8
           ||  |:|
Db     320 DDYGHIR 326
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Result No.	Score	Query Match	Length	DB	ID	Description
1	52	96.3	11	2	A60656	perisulfakinin - A
2	52	96.3	14	2	A56632	neosulfakinin-II -
3	52	96.3	128	2	A31102	drosulfakinin prec
4	52	96.3	140	2	S66610	sulfakinin - blueb
5	48	88.9	11	1	GMROL	leucosulfakinin -
6	46	85.2	10	1	GMROL2	leucosulfakinin-II
7	46	85.2	10	2	B60656	leucosulfakinin II
8	40	74.1	35	2	B48682	G protein-coupled
9	40	74.1	590	1	A54372	G protein-coupled
10	40	74.1	590	2	A48277	G protein-coupled
11	39	72.2	310	2	B86825	aspartate carbamoy
12	39	72.2	345	2	B83371	conserved hypothet
13	39	72.2	419	2	S72325	glucan 1,3-beta-gl
14	39	72.2	471	2	B97611	UDP-N-acetylmurama
15	39	72.2	471	2	AF2833	UDP-N-acetylmurama

RESULT 1
A60656
perisulfakinin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 11-Jul-1997
C;Accession: A60656
R;Veenstra, J.A.
Neuropeptides 14, 145-149, 1989
A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.
A;Reference number: A60656; MUID:90137190
A;Accession: A60656
A;Molecule type: protein
A;Residues: 1-11 <VEE>
C;Comment: This neuropeptide stimulates hindgut contractions.
C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F,6/Binding site: sulfate (Tyr) (covalent) #status experimental
F,11/Modified site. amidated carboxyl end (Phe) #status experimental

Query Match 96.3%; Score 52; DB 2; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.0013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 FDDYGHLRF 9
           ||||||:||
Db       3 FDDYGHMRF 11
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RESULT 2
A56632
neosulfakinin-II - flesh fly (Sarcophaga bullata)
N;Alternate names: Neb-SK-II

N,Contains: neosulfakinin-I (Neb-SK-I)
C,Species: Sarcophaga bullata
C,Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C,Accession: A56632
R,Fonagy, A.; Schoofs, L.; Proost, P ; Van Damme, J.; De Loof, A
Comp. Biochem Physiol. C 103, 135-142, 1992
A,Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshfly, Neobellieria bullata.
A,Reference number: A56632; MUID:93083101
A,Accession: A56632
A,Molecule type: protein
A,Residues: 1-14 <FON>
A,Experimental source: heads
A,Note: sequence extracted from NCBI backbone (NCBIP:120391)
C,Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F,1-14/Product: neosulfakinin-II #status experimental <NSK2>
F,6-14/Product: neosulfakinin-I #status experimental <NSK1>
F,9/Binding site: sulfate (Tyr) (covalent) #status predicted
F,14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 96.3%; Score 52; DB 2; Length 14;
Best Local Similarity 88.9%; Pred. No. 0.0016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 FDDYGHLRF 9
           ||| ||:|:
Db       6 FDDYGHMRF 14
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	96.3	9	1	NSK1_SARBU	P41492 sarcophaga
2	52	96.3	11	1	LSKP_PERAM	P36885 periplaneta
3	52	96.3	14	1	NSK2_SARBU	P41493 sarcophaga
4	52	96.3	128	1	DSK_DROME	P09040 drosophila
5	48	88.9	11	1	LSK1_LEUMA	P04428 leucophaea
6	46	85.2	10	1	LSK2_LEUMA	P09039 leucophaea
7	46	85.2	12	1	LOSK_LOCMI	P47733 locusta mig
8	40	74.1	590	1	GRK5_BOVIN	P43249 bos taurus
9	40	74.1	590	1	GRK5_HUMAN	P34947 homo sapien
10	40	74.1	590	1	GRK5_RAT	Q62833 rattus norv
11	39	72.2	310	1	PYPB_LACLA	Q9cf79 lactococcus
12	38	70.4	182	1	RL5_SULSO	Q9ux93 sulfolobus
13	38	70.4	463	1	FLGE_TREPH	Q56326 treponema p
14	37	68.5	190	1	RL5_METJA	P54040 methanococc
15	37	68.5	1144	1	CYA3_HUMAN	O60266 homo sapien
16	37	68.5	1144	1	CYA3_RAT	P21932 rattus norv
17	36	66.7	200	1	YCLP_XANCP	P22264 xanthomonas
18	36	66.7	214	1	VC01_VARV	P33859 variola vir
19	36	66.7	224	1	VC01_VACCC	P21036 vaccinia vi
20	36	66.7	229	1	VC01_VACCV	P17368 vaccinia vi
21	36	66.7	454	1	MURC_AQUAE	O67373 aquifex aeo
22	35	64.8	576	1	GRK6_HUMAN	P43250 homo sapien
23	35	64.8	576	1	GRK6_MOUSE	O70293 mus musculu
24	35	64.8	576	1	GRK6_RAT	P97711 rattus norv
25	35	64.8	642	1	YQR1_CAEEL	Q09537 caenorhabdi

RESULT 1
NSK1_SARBU
ID NSK1_SARBU STANDARD; PRT; 9 AA.
AC P41492;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

```
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   Neosulfakinin-I (NEB-SK-I).
OS   Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Oestroidea; Sarcophagidae; Sarcophaga
OX   NCBI_TaxID=7385;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RX   MEDLINE=93083101; PubMed=1360367,
RA   Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT   "Isolation and primary structure of two sulfakinin-like peptides from
RT   the fleshfly, Neobellieria bullata.";
RL   Comp. Biochem. Physiol. 103C:135-142(1992).
CC   -!- FUNCTION: MYOTROPIC PEPTIDE.
CC   -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; 1.
KW   Neuropeptide; Amidation; Sulfation.
FT   MOD_RES       4      4       SULFATION (POTENTIAL).
FT   MOD_RES       9      9       AMIDATION (POTENTIAL).
SQ   SEQUENCE   9 AA;  1187 MW;  8B0A0691E86B5AAA CRC64;


  Query Match             96.3%;  Score 52,  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1e+05;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 FDDYGHLRF 9
           !||||:||
Db       1 FDDYGHMRF 9
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SUMMARIES

Result No	Score	% Query Match	Length	DB	ID	Description
1	40	74.1	590	11	O70292	O70292 mus musculu
2	40	74.1	590	11	O70297	O70297 mus musculu
3	39	72.2	255	5	Q9VIT0	Q9vit0 drosophila
4	39	72.2	310	2	Q9L4N6	Q9l4n6 lactococcus
5	39	72.2	345	16	Q9I1S0	Q9i1s0 pseudomonas
6	39	72.2	419	3	Q12539	Q12539 agaricus bi
7	39	72.2	420	3	Q9C1A8	Q9c1a8 gibberella
8	39	72.2	420	3	Q9C1B5	Q9c1b5 fusarium sp
9	39	72.2	420	3	Q96V36	Q96v36 gibberella
10	39	72.2	466	16	Q98KB4	Q98kb4 rhizobium l
11	39	72.2	471	16	Q92NM0	Q92nm0 rhizobium m
12	39	72.2	477	5	P91348	P91348 caenorhabdi
13	38	70.4	174	16	Q92JL8	Q92jl8 rickettsia
14	38	70.4	281	5	Q9V3A9	Q9v3a9 drosophila
15	38	70.4	1186	3	Q12466	Q12466 saccharomyc
16	37	68.5	323	5	Q9GUN9	Q9gun9 caenorhabdi

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RESULT   1
O70292
ID   O70292      PRELIMINARY;      PRT;   590 AA.
AC   O70292;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   G PROTEIN-COUPLED RECEPTOR KINASE 5.
GN   GPRK5 OR GRK5.
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99436149; PubMed=10506199;
RA   Premont R.T., Macrae A.D., Aparicio S.A., Kendall H.E., Welch J.E.,
RA   Lefkowitz R.J.;
RT   "The GRK4 subfamily of G protein-coupled receptor kinases. Alternative
RT   splicing, gene organization, and sequence conservation.";
RL   J. Biol. Chem. 274:29381-29389(1999).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. GPRK
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR   EMBL; AF040746; AAC09267.1; -.
DR   HSSP; Q63450; 1A06.
DR   MGD; MGI:109161; Gprk5.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000239; GPCR_kinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000342; RGS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00615; RGS; 1.
DR   PRINTS; PR00717; GPCRKINASE.
DR   SMART; SM00315; RGS; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50132; RGS; 1.
KW   ATP-binding; Kinase; Receptor; Transferase.
SQ   SEQUENCE   590 AA;  67732 MW;  F47D87397B1A2399 CRC64;


  Query Match             74.1%;  Score 40;  DB 11;  Length 590;
  Best Local Similarity   85.7%;  Pred. No. 40;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 DDYGHLR 8
           ||  |:
Db     320 DDYGHIR 326


RESULT   2
Q70297
ID   Q70297      PRELIMINARY;      PRT;   590 AA.
AC   Q70297;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   G PROTEIN-COUPLED RECEPTOR KINASE 5.
GN   GPRK5 OR GRK5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SVJ;
RX   MEDLINE=99436149; PubMed=10506199;
RA   Premont R.T., Macrae A.D., Aparicio S.A., Kendall H.E., Welch J.E.,
RA   Lefkowitz R.J.;
RT   "The GRK4 subfamily of G protein-coupled receptor kinases. Alternative
RT   splicing, gene organization, and sequence conservation.";
RL   J. Biol. Chem. 274:29381-29389(1999).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. GPRK
CC       SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR   EMBL; AF040759; AAC09271.1; -.
DR   EMBL; AF040755; AAC09271.1; JOINED.
DR   EMBL; AF040756; AAC09271.1; JOINED.
DR   EMBL; AF040757; AAC09271.1; JOINED.
DR   EMBL; AF040758; AAC09271.1; JOINED.
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DR HSSP; Q63450; 1A06.
DR MGD; MGI:109161; Gprk5.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000239; GPCR_kinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000342; RGS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR00717; GPCRKINASE.
DR SMART; SM00315; RGS; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50132; RGS; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 590 AA; 67796 MW; 22253281964DEF64 CRC64;

Query Match 74.1%; Score 40; DB 11; Length 590;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 DDYGHLR 8
           |||||:|
Db     320 DDYGHIR 326
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NEWS 4	Feb 01	DKILIT now produced by FIZ Karlsruhe and has a new update frequency
NEWS 5	Feb 19	Access via Tymnet and SprintNet Eliminated Effective 3/31/02
NEWS 6	Mar 08	Gene Names now available in BIOSIS
NEWS 7	Mar 22	TOXLIT no longer available
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NEWS 9	Mar 28	US Provisional Priorities searched with P in CA/CAplus and USPATFULL
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NEWS 16	Apr 22	Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
NEWS 17	Apr 22	BIOSIS Gene Names now available in TOXCENTER
NEWS 18	Apr 22	Federal Research in Progress (FEDRIP) now available
NEWS 19	Jun 03	New e-mail delivery for search results now available
NEWS 20	Jun 10	MEDLINE Reload
NEWS 21	Jun 10	PCTFULL has been reloaded
NEWS 22	Jul 02	FOREGE no longer contains STANDARDS file segment
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NEWS 24	Jul 22	USAN to be reloaded July 28, 2002; saved answer sets no longer valid

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=> s dmgpcr

L1 1 DMGPCR

=> s drosophila (p) receptor (p) coupled (p) bind

L2 51 DROSOPHILA (P) RECEPTOR (P) COUPLED (P) BIND

=> dup rem l2

PROCESSING COMPLETED FOR L2
L3 18 DUP REM L2 (33 DUPLICATES REMOVED)

=> d l3 total ibib kwic

L3 ANSWER 1 OF 18 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002045994 IN-PROCESS
DOCUMENT NUMBER: 21630175 PubMed ID: 11754840
TITLE: Regulation of the Rhodopsin Protein Phosphatase, RDGC, through Interaction with Calmodulin.
AUTHOR: Lee S J; Montell C
CORPORATE SOURCE: Department of Biological Chemistry and, Department of Neuroscience, The Johns Hopkins University School of Medicine, 21205, Baltimore, MD, USA.
SOURCE: NEURON, (2001 Dec 20) 32 (6) 1097-106.
Journal code: 8809320. ISSN: 0896-6273.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020124
Last Updated on STN: 20020124
AB Hundreds of G protein-**coupled receptors** (GPCRs) and at least six GPCR kinases have been identified, but the only GPCR phosphatase

that has been definitively demonstrated is the rhodopsin phosphatase encoded by the rdgC locus of **Drosophila**. Mutations in rdgC result in defects in termination of the light response and cause severe retinal degeneration. In the current work, we demonstrate that RDGC **binds** to calmodulin, and a mutation in an IQ motif that eliminates the calmodulin/RDGC interaction prevents dephosphorylation of rhodopsin in vivo. . .

L3 ANSWER 2 OF 18 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:244124 BIOSIS
DOCUMENT NUMBER: PREV200100244124
TITLE: The 1.8ANG crystal structure of InaD PDZ1 complexed with its peptide target reveals a novel mode of PDZ domain binding.
AUTHOR(S): Pliske, Michelle (1); Sondek, John (1)
CORPORATE SOURCE: (1) Biochemistry and Biophysics, UNC-Chapel Hill, Mary Ellen Jones Bldg., Chapel Hill, NC, 27599 USA
SOURCE: FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A723. print.
Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology 2001 Orlando, Florida, USA March 31-April 04, 2001
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB **Drosophila** phototransduction is a model system for the study of G-protein **coupled** phospholipase-C (PLC) signaling pathways in complex organisms. In this cascade light activates the seven-transmembrane **receptor** rhodopsin, which in turn activates Gq, allowing its dissociation into signaling-competent alpha and betagamma subunits. Gqalpha induces the PLC-beta4 homolog no **receptor** potential A (norpA) to cleave phosphatidylinositol-4,5-bisphosphate (PIP2) to the second messengers inositol tri-phosphate (IP3) and diacylglycerol (DAG), leading to the. . . multi-domain scaffolding protein inactivation no after-potential D (inaD). InaD contains five tandem PDZ protein interaction domains, each of which can **bind** one or multiple phototransduction proteins. PDZ domains **bind** to the extreme carboxy-terminal (C-terminal) three amino acids of their targets, including the free carboxyl group. InaD PDZ1 **binds** to norpA, whose C-terminal sequence is FCA. The X-ray crystal structure of PDZ1 bound to a norpA C-terminal heptapeptide was. . .

L3 ANSWER 3 OF 18 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:492061 BIOSIS
DOCUMENT NUMBER: PREV200100492061
TITLE: Comparison of adenylyl cyclase stimulation by 5-HT4(b) and 5-HT7(a) receptors using the Ecdysone-Inducible Mammalian Expression System.
AUTHOR(S): Bruheim, S. (1); Andressen, K. W. (1); Krobert, K. A. (1); Levy, F. O. (1)
CORPORATE SOURCE: (1) MSD Cardiovascular Res. Ctr. and Dept. of Pharmacol., Univ. of Oslo, Oslo Norway
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 690. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The serotonin (5-HT) **receptors** 5-HT4 and 5-HT7 are G-protein

coupled receptors that activate adenylyl cyclase (AC) and exist in several splice variants differing only in their intracellular carboxyl terminal tails. We wanted to determine if activation of AC differed between the 5-HT4(b) and 5-HT7(a) **receptors**. Comparison of **receptor** function using constitutive expression systems can be confounded by different **receptor** expression levels and clonal cell line differences. By using the Ecdysone-Inducible Mammalian Expression System we could reproducibly express varying levels of **receptor** in the same clonal cell line. This system utilizes a heterodimer (VgRxR) of the modified ecdysone **receptor** (VgEcR) from **Drosophila** and the retionoid X **receptor** (RXR). This **receptor binds** a hybrid ecdysone response element (E/GRE) in the presence of the synthetic analog of ecdysone, ponasterone A. HEK293 cells stably expressing the heterodimer VgRxR **receptor** were stably transfected with a vector containing the coding regions for 5-HT4(b) and 5-HT7(a) **receptors** downstream of the E/GRE. Radioligand binding revealed low constitutive expression of both **receptors**, which could be titrated up to 3.7 pmol/mg protein with ponasterone A. Preliminary data indicate that constitutive AC activity and potency (EC50) of 5-HT are **receptor** level dependent at the 5-HT4(b) **receptor** but not at the 5-HT7(a) **receptor**. Additionally, the 5-HT7(a) **receptor** activated AC more efficiently than the 5-HT4(b) **receptor** over a wide range of expression levels. Comparative studies on inverse agonism are ongoing.

L3 ANSWER 4 OF 18 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001271685 MEDLINE
DOCUMENT NUMBER: 21261850 PubMed ID: 11369206
TITLE: Mutations in the sterol-sensing domain of Patched suggest a role for vesicular trafficking in Smoothened regulation.
COMMENT: Erratum in: Curr Biol 2001 Jul 24;11(14):1153
AUTHOR: Strutt H; Thomas C; Nakano Y; Stark D; Neave B; Taylor A M; Ingham P W
CORPORATE SOURCE: MRC Intercellular Signalling Group, Centre for Developmental Genetics, Department of Biomedical Science, University of Sheffield, Sheffield, United Kingdom.
SOURCE: CURRENT BIOLOGY, (2001 Apr 17) 11 (8) 608-13. Journal code: 9107782. ISSN: 0960-9822.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20010813
Entered Medline: 20010809

AB The tumor suppressor gene patched (ptc) encodes an approximately 140 kDa polytopic transmembrane protein [1-3] [corrected] that **binds** members of the Hedgehog (Hh) family of signaling proteins [4-6] [corrected] and regulates the activity of Smoothened (Smo), a G protein-**coupled receptor**-like protein essential for Hh signal transduction [7-9] [corrected]. Ptc contains a sterol-sensing domain (SSD) [10, 11] [corrected], a motif found. . . (Hh) signaling by facilitating the regulated secretion and sequestration of the Hh protein [16] [corrected], to which it is covalently **coupled**. In addition, cholesterol synthesis inhibitors block the ability of cells to respond to Hh [18, 19] [corrected], and this finding. . . has so far been lacking.
Here we describe the identification and characterization of two missense mutations in the SSD of **Drosophila** Ptc; strikingly, while both

mutations abolish Smo repression, neither affects the ability of Ptc to interact wit[redacted]dh. We speculate. . .

L3 ANSWER 5 OF 18 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002053834 MEDLINE
DOCUMENT NUMBER: 21638057 PubMed ID: 11779634
TITLE: The transcription factors Sp1 and Sp3 are required for human angiotensin II type 1 receptor gene expression in H295-R cells.
AUTHOR: Zhao X; Martin M M; Elton T S
CORPORATE SOURCE: Department of Chemistry and Biochemistry, Brigham Young University, C206 Benson Building, P.O. Box 25700, Provo, UT
84602-5700, USA.
CONTRACT NUMBER: HL48848 (NHLBI)
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2001 Dec 30) 1522 (3) 195-206.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020222
Entered Medline: 20020221
AB . . . peptide hormone angiotensin II regulates a variety of physiological responses which are mediated by its interaction with high affinity G protein-**coupled receptors** localized on the surface of target cells. Our previous studies have demonstrated that a 145
bp sequence within the promoter region was required for basal level expression of the human angiotensin II type 1 **receptor** (hAT(1)R) gene. In the present study, deletional analysis of the hAT(1)R promoter localized the major regulatory sequence to two overlapping. . . binding
site for Sp1 prevented the formation of the DNA-protein complexes. Supershift EMSAs also demonstrated that Sp1 and Sp3 could **bind** to the GC boxes present within the -105 to -85 bp region of the hAT(1)R promoter. Transactivation experiments utilizing **Drosophila** SL2 cells, which lack endogenous Sp family transcription factors, demonstrated
that Sp1 and Sp3 activated the hAT(1)R promoter and that. . .

L3 ANSWER 6 OF 18 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001688270 MEDLINE
DOCUMENT NUMBER: 21592298 PubMed ID: 11734218
TITLE: Identification of mouse trp homologs and lipid rafts from spermatogenic cells and sperm.
AUTHOR: Trevino C L; Serrano C J; Beltran C; Felix R; Darszon A
CORPORATE SOURCE: Department of Genetics and Molecular Physiology, Institute of Biotechnology, UNAM, Cuernavaca, Mexico.
SOURCE: FEBS LETTERS, (2001 Nov 30) 509 (1) 119-25.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011206
Last Updated on STN: 20020125
Entered Medline: 20020122
AB . . . of the membrane systems that regulate Ca(2+) in sperm. In this report, we provide evidence for the expression of seven **Drosophila** transient **receptor** potential homolog genes (trp1-7) and three of their protein products (Trp1, Trp3 and Trp6) in mouse sperm. Allegedly

some trps. . . . major component of caveolae, a subset of lipid rafts potentially important for signaling events and Ca(2+) flux. Furthermore, by using fluorescein-**coupled** cholera toxin B subunit, which specifically **binds** to the raft component ganglioside GM1, we identified caveolin- and Trp-independent lipid rafts residing in the plasma membrane of mature. . .

L3 ANSWER 7 OF 18 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:297449 CAPLUS
DOCUMENT NUMBER: 130:321591
TITLE: Cloning and cDNA sequence of an invertebrate octopamine receptor
INVENTOR(S): Davis, Ronald L.; Han, Kyung-an; Millar, Neil S.
PATENT ASSIGNEE(S): Baylor College of Medicine, USA
SOURCE: PCT Int. Appl., 58 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9921891	A1	19990506	WO 1998-US22808	19981027
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9919008	A1	19990517	AU 1999-19008	19981027

PRIORITY APPLN. INFO.: US 1997-63391P P 19971027
WO 1998-US22808 W 19981027
REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE
FORMAT
AB The present invention provides a novel octopamine **receptor** comprised of an invertebrate **receptor** which **binds** octopamine and is **coupled** to adenylyl cyclase system. The invention also includes methods of using the octopamine **receptor** to screen for agonists, antagonists and pesticides. In this method the octopamine **receptor** is inserted into invertebrate or vertebrate cells, test compd. is added and the activity of the octopamine **receptor coupled** to the adenylyl cyclase system or the internal Ca2+ system is measured. Also included is an expression system for prodn. of the octopamine **receptor**. The octopamine **receptor** cDNA was cloned from **Drosophila** melanogaster using PCR and single-strand conformation polymorphism.

L3 ANSWER 8 OF 18 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 1999147062 MEDLINE
DOCUMENT NUMBER: 99147062 PubMed ID: 10022914
TITLE: Identification of a novel family of targets of PYK2 related to Drosophila retinal degeneration B (rdgB) protein.
AUTHOR: Lev S; Hernandez J; Martinez R; Chen A; Plowman G; Schlessinger J
CORPORATE SOURCE: Sugen, Inc., South San Francisco, California 94080, USA.
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (1999 Mar) 19 (3) 2278-88.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990402
Last Updated on STN: 19990402
Entered Medline: 19990325

AB The protein tyrosine kinase PYK2 has been implicated in signaling pathways activated by G-protein-**coupled receptors**, intracellular calcium, and stress signals. Here we describe the molecular cloning and characterization of a novel family of PYK2-binding proteins designated Nirs (PYK2 N-terminal domain-interacting **receptors**). The three Nir proteins (Nir1, Nir2, and Nir3) **bind** to the amino-terminal domain of PYK2 via a conserved sequence motif located in the carboxy terminus. The primary structures of. . . region homologous to phosphatidylinositol (PI) transfer protein, and an acidic domain. The Nir proteins are the human homologues of the **Drosophila** retinal degeneration B protein (rdgB), a protein implicated in the visual transduction pathway in flies. We demonstrate that Nirs are. . . family of evolutionarily conserved PYK2-binding proteins that play a role in the control of calcium and phosphoinositide metabolism downstream of G-protein-**coupled receptors**.

L3 ANSWER 9 OF 18 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 1998227978 MEDLINE
DOCUMENT NUMBER: 98227978 PubMed ID: 9569023
TITLE: Disabled-2 (Dab2) is an SH3 domain-binding partner of Grb2.
AUTHOR: Xu X X; Yi T; Tang B; Lambeth J D
CORPORATE SOURCE: Department of Biochemistry, and Winship Cancer Center, Emory University School of Medicine, Atlanta, Georgia 30322, USA.
CONTRACT NUMBER: R 01 CA75389-01 (NCI)
R01CA46508 (NCI)
SOURCE: ONCOGENE, (1998 Mar 26) 16 (12) 1561-9.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980520
Last Updated on STN: 20000303
Entered Medline: 19980513

AB Disabled-2 (Dab2), a mammalian structural homolog of **Drosophila** Disabled (Dab), is a mitogen-responsive phosphoprotein. It has been speculated to be a negative regulator of growth since its expression. . . . exchange factor for Ras. The proline-rich sequences of Sos mediate the interaction of Sos with Grb2, an adaptor protein which **coupled** tyrosine kinase **receptors** to Sos. Herein, we have investigated the possibility that Dab2 interacts with Grb2. In experiments of co-immunoprecipitation from BAC1.2F5 macrophage. . . disrupting the Grb2-Sos complex. The expressed proline-rich domain of Dab2 (#600-730) bound Grb2, but other regions of Dab2 failed to **bind** Grb2. Both of the individual SH3 domains of Grb2 bound to Sos (N-terminal SH3 domain >> C-terminal SH3 domain), but. . . to Dab2 required the intact Grb2, suggesting cooperative binding using both SH3 domains of Grb2. These data indicate that Dab2 **binds** to the SH3 domains of Grb2 via its C-terminal proline-rich sequences. Dab2 may modulate growth factor/Ras pathways by competing with. . .

L3 ANSWER 10 OF 18 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 1998340528 MEDLINE
DOCUMENT NUMBER: 98340528 PubMed ID: 9675877
TITLE: The c-Cbl oncoprotein.
AUTHOR: Lupher M L Jr; Andoniou C E; Bonita D; Miyake S; Band H
CORPORATE SOURCE: Department of Medicine, Brigham and Women's Hospital,

Harvard Medical School, Boston, MA 02115, USA.
SOURCE: INTERNATIONAL JOURNAL OF BIOCHEMISTRY AND CELL BIOLOGY, (1998 Apr) 30 (4) 439-44. Ref: 16
Journal code: 9508482. ISSN: 1357-2725.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980820
Last Updated on STN: 19980820
Entered Medline: 19980813

AB Cbl has emerged as a novel signal transducing protein downstream of a number of cell surface **receptors coupled** to tyrosine kinases. Identified as the protein product of the c-cbl proto-oncogene, the cellular homolog to the transforming gene of. . . finger render Cbl oncogenic, whereas wild type Cbl is non-transforming, even if overexpressed. Cbl serves as a substrate of both **receptor** and non-**receptor** tyrosine kinases, and **binds** to adaptor proteins Grb2, Crk and the p85 subunit of PI-3-kinase. Additionally, both Caenorhabditis elegans and **Drosophila** Cbl homologs, SLI-1 and D-Cbl, respectively, have been identified as negative regulators of the LET-23/DER **receptor** tyrosine kinases. Finally, oncogenic mutants of Cbl, when expressed in fibroblasts, upregulate the signaling cascade downstream of the platelet-derived growth factor **receptor** alpha in a Cbl-PTB domain-dependent manner. Together, these findings position Cbl as a central player in the regulation of tyrosine. . .

L3 ANSWER 11 OF 18 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:340756 BIOSIS
DOCUMENT NUMBER: PREV199900340756
TITLE: First Annual Jorge Chevesich Memorial Lecture: A supramolecular signaling complex required for Drosophila visual transduction.
AUTHOR(S): Montell, Craig (1)
CORPORATE SOURCE: (1) Departments of Biological Chemistry and Neuroscience, Johns Hopkins University School of Medicine, 725 N. Wolfe Street, Baltimore, MD, 21205 USA
SOURCE: Einstein Quarterly Journal of Biology and Medicine, (1998) Vol. 15, No. 4, pp. 198-211.
ISSN: 0724-6706.
DOCUMENT TYPE: General Review
LANGUAGE: English
SUMMARY LANGUAGE: English

AB **Drosophila** phototransduction represents one of the fastest known G-protein **coupled** signaling cascades. Exposure of the photoreceptor cells to light leads to activation of the light-induced cation influx channels, TRP and. . . in phototransduction are linked into a supramolecular signaling complex (signalplex) has led to a reevaluation of the mechanisms underlying the **Drosophila** photoresponse. The central player is INAD, a protein with five protein interaction motifs referred to as PDZ domains. At least seven signaling molecules **bind** to INAD. These include rhodopsin, phospholipase C-beta, protein kinase C, TRP, TRPL, calmodulin and an unconventional myosin, NINAC. Someof the. . . Since more than five proteins interact with INAD, it would appear that a single INAD monomer lacks the capacity to **bind** to each of its targets simultaneously. The finding that INAD is capable of forming homo-multimers in vitro raises the possibility that the entire phototransduction cascade may be physically **coupled** in the signalplex. Nearly all of the proteins that function in the signalplex have known vertebrate homologs. These include a. . . neurons of the central nervous system around the time of birth. TRPC3 appears to be activated through stimulation of the **receptor**

tyrosine kinase, TrkB, and phospholipase C-gamma. Thus, a variety of pathways leading to the stimulation of phospholipase C appear to. . .

L3 ANSWER 12 OF 18 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 1998024192 MEDLINE
DOCUMENT NUMBER: 98024192 PubMed ID: 9356510
TITLE: Association of INAD with NORPA is essential for controlled activation and deactivation of Drosophila phototransduction in vivo.
AUTHOR: Shieh B H; Zhu M Y; Lee J K; Kelly I M; Bahiraei F
CORPORATE SOURCE: Department of Pharmacology, Vanderbilt University, Nashville, TN 37232-6600, USA.. shiehb@ctrvax.vanderbilt.edu
CONTRACT NUMBER: EY09743 (NEI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1997 Nov 11) 94 (23) 12682-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971216

AB Visual transduction in **Drosophila** is a G protein-**coupled** phospholipase C-mediated process that leads to depolarization via activation of the transient **receptor** potential (TRP) calcium channel. Inactivation-no-afterpotential D (INAD) is an adaptor protein containing PDZ domains known to interact with TRP. Immunoprecipitation studies indicate that INAD also **binds** to eye-specific protein kinase C and the phospholipase C, no-**receptor**-potential A (NORPA). By overlay assay and site-directed mutagenesis we have defined the essential elements of the NORPA-INAD association and identified. .

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L3 ANSWER 13 OF 18 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 97197784 MEDLINE
DOCUMENT NUMBER: 97197784 PubMed ID: 9045634
TITLE: Cloning and expression of a complementary DNA encoding a molluscan octopamine receptor that couples to chloride channels in HEK293 cells.
AUTHOR: Gerhardt C C; Lodder H C; Vincent M; Bakker R A; Planta R J; Vreugdenhil E; Kits K S; van Heerikhuizen H
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Research Institute Neurosciences, Vrije Universiteit, De Boelelaan 1083, 1081 HV Amsterdam, The Netherlands.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Mar 7) 272 (10) 6201-7. Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U62770
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970424
Last Updated on STN: 20000303
Entered Medline: 19970414

AB A cDNA encoding a G-protein-**coupled receptor** was cloned from the central nervous system of the pond snail Lymnaea stagnalis. The predicted amino acid sequence of this cDNA most closely resembles the **Drosophila** tyramine/octopamine **receptor**, the Locusta tyramine **receptor**, and an octopamine **receptor** (Lym oa1) that we recently cloned from Lymnaea. After

stable expression of the cDNA in HEK293 cells, we found that [3H]rauwolsc[redacted] **binds** with high affinity to t[redacted] **receptor** (KD = 6.2.10(-9) M). Octopamine appears to be the most potent naturally occurring agonist to displace the [3H]rauwolscine binding (Ki = 3.0.10(-7) M). Therefore, the **receptor** is considered to be an octopamine **receptor** and is consequently designated Lym oa2. The novel **receptor** shares little pharmacological resemblance with Lym oa1, indicating that the two **receptors** represent different octopamine **receptor** subfamilies. Octopaminergic stimulation of Lym oa2 does not induce changes in intracellular concentrations of cAMP or inositol phosphates. However, electrophysiological. . .

L3 ANSWER 14 OF 18 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 97472416 MEDLINE
DOCUMENT NUMBER: 97472416 PubMed ID: 9333241
TITLE: Prolonged photoresponses in transgenic mouse rods lacking arrestin.
AUTHOR: Xu J; Dodd R L; Makino C L; Simon M I; Baylor D A; Chen J
CORPORATE SOURCE: Division of Biology, California Institute of Technology, Pasadena 91125, USA.
SOURCE: NATURE, (1997 Oct 2) 389 (6650) 505-9.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199710
ENTRY DATE: Entered STN: 19971105
Last Updated on STN: 19971105
Entered Medline: 19971022

AB Arrestins are soluble cytoplasmic proteins that **bind** to G-protein-**coupled receptors**, thus switching off activation of the G protein and terminating the signalling pathway that triggers the cellular response. Although visual. . . was halved, indicating that arrestin binding is not rate limiting for recovery of the rod photoresponse, as it is in **Drosophila**. With arrestin absent, the flash response displayed a rapid partial recovery followed by a prolonged final phase. This behaviour indicates. . .

L3 ANSWER 15 OF 18 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 97347296 MEDLINE
DOCUMENT NUMBER: 97347296 PubMed ID: 9203635
TITLE: Molecular cloning and pharmacological characterization of a molluscan octopamine receptor.
AUTHOR: Gerhardt C C; Bakker R A; Piek G J; Planta R J; Vreugdenhil E; Leysen J E; Van Heerikhuizen H
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, Research Institute Neurosciences, Vrije Universiteit, Amsterdam, The Netherlands.
SOURCE: MOLECULAR PHARMACOLOGY, (1997 Feb) 51 (2) 293-300.
Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199707
ENTRY DATE: Entered STN: 19970805
Last Updated on STN: 19970805
Entered Medline: 19970723

AB We describe the cloning and functional expression of a cDNA encoding a novel G protein-**coupled receptor**, which was isolated from the central nervous system of the pond snail Lymnaea stagnalis. The

amino acid sequence predicted by this cDNA shows highest similarity with the sequence of the Locusta tyramine **receptor**, the **Drosophila** tyramine/octopamine **receptor**, and the mammalian alpha-adrenergic **receptors**. On expression in mammalian cells, [3H]rauwolscine, an alpha2-adrenergic **receptor** antagonist, **binds** with high affinity (K(D) = 2.9 x 10(-9) M) to the **receptor**. Of several tested neurotransmitters, octopamine (which is considered to be the invertebrate counterpart of norepinephrine) showed the highest affinity (1.9 x 10(-6) M) for the **receptor**. Therefore, we consider this **receptor** to be the first true octopamine **receptor** to be cloned. The ligand binding properties of the novel **receptor**, designated Lym oa1, seem to be distinct from any of the binding profiles described for octopamine **receptors** in tissue preparations. Although the pharmacological profile of Lym oa1 shows some similarity with that of Tyr/Oct-Dro and Tyr-Loc, there. . . also clear differences. In particular, phentolamine, chlorpromazine, and mianserine display markedly higher affinities for Lym oa1 than for the insect **receptors**. As far as the vertebrate adrenergic **receptors** are concerned, the ligand binding properties of Lym oa1 resemble alpha2-adrenergic **receptors** more than they do alpha- or beta-adrenergic **receptors**. Octopaminergic stimulation of Lym oa1 induces an increase in both inositol phosphates and cAMP (EC50 = 9.1 x 10(-7) M. . . x 10(-6) M, respectively). This is in contrast to the signal transduction pathways described for the related tyramine- and alpha2-adrenergic **receptors**, which couple in an inhibitory way to adenylyl cyclase.

L3 ANSWER 16 OF 18 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 91198639 MEDLINE
DOCUMENT NUMBER: 91198639 PubMed ID: 1849770
TITLE: Very high affinity interaction of DPI 201-106 and BDF 8784 enantiomers with the phenylalkylamine-sensitive Ca2(+)-channel in Drosophila head membranes.
AUTHOR: Glossmann H; Zech C; Striessnig J; Staudinger R; Hall L; Greenberg R; Armah B I
CORPORATE SOURCE: Institut fur Biochemische Pharmakologie, Innsbruck, Austria.
SOURCE: BRITISH JOURNAL OF PHARMACOLOGY, (1991 Feb) 102 (2) 446-52.
Journal code: 7502536. ISSN: 0007-1188.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199105
ENTRY DATE: Entered STN: 19910607
Last Updated on STN: 19970203
Entered Medline: 19910523

AB 1. Piperazinylindoles (DPI 201-106, BDF 8784), drugs known to act on voltage-dependent Na(+)-channels, **bind** with very high affinity to a Ca2(+)-channel-associated phenylalkylamine **receptor** in **Drosophila** melanogaster head membranes. These compounds and (+)-tetrandrine, a naturally occurring Ca2(+)-antagonist, were the most selective inhibitors for phenylalkylamine-labelled **Drosophila** Ca2(+)-channels compared to mammalian L-type Ca2(+)-channels. 2. Replacement of the cyano group by a methyl group in (+)-DPI 201-106 ((+)-BDF 8784) increases the IC50 value for inhibition of phenylalkylamine labelling of **Drosophila** Ca2(+)-channels from 0.29 to 2.1 nM but decreases the IC50 value for inhibition of phenylalkylamine labelling of mammalian skeletal muscle. . . to 49 nM. 3. DPI 201-106 enantiomers completely block (at 0.1 microM) phenylalkylamine photolabelling of a 136 K polypeptide in **Drosophila** head membranes whereas 10 microM aconitine or lidocaine are without effect. 4. Assessment of the

Ca2(+)-antagonist effects of the substituted. . . and chemical selectivity [redacted] related to local anaesthetic ac[redacted]ity. 6. It is proposed that a very high affinity piperazinylindole-selective site is **coupled** to the phenylalkylamine **receptor** of **Drosophila** Ca2(+)-channels. These sites are still present on mammalian L-type Ca2(+)-channels but have lower affinity and/or are less tightly **coupled** to phenylalkylamine **receptors** on the alpha 1-subunit.

L3 ANSWER 17 OF 18 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:224365 BIOSIS
DOCUMENT NUMBER: BA87:115982
TITLE: STRUCTURE-MEMBRANE MECHANISM OF DISTANT REGULATION OF INTERCELLULAR GAP JUNCTION PERMEABILITY.
AUTHOR(S): MAZHUL' V M; KONEV S V; YANCHEVSKAYA T G; FININ V S
CORPORATE SOURCE: INST. PHOTOBIOL., ACAD. SCI. B. SSR, MINSK, USSR.
SOURCE: BIOFIZIKA, (1989) 33 (6), 1023-1028.
CODEN: BIOFAI. ISSN: 0006-3029.
FILE SEGMENT: BA; OLD
LANGUAGE: Russian
AB. . . shown by ESR and tryptophane fluorescence at room temperature that concanavalin A (Con A) at a concentration of 10 mg/ml **binds** with glycoprotein **receptors** on the surface of salivary gland cells of **Drosophila** virilis larva beyong gap junction regions initiating generalized structural reorganization of plasmic membranes. The reorganization is **coupled** with a decrease in permeability of intercellular channels to small inorganic ions and molecules of the organic dye fluorescein. Treatment. . . structural and functional effects were reversible and nullified by substituting 4 mM .alpha.-D-glucopyronoside for lecitin in cell surface receptors. The **obtained** results suggest the existence of a structural membrane mechanism of distant regulation of intercellular communications according to the following pattern:. . .

L3 ANSWER 18 OF 18 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:92520 CAPLUS
DOCUMENT NUMBER: 110:92520
TITLE: Structure-membrane mechanism of distant regulation of intercellular gap junction permeability
AUTHOR(S): Mazhul, V. M.; Konev, S. V.; Yanchevskaya, T. G.; Phinin, V. S.
CORPORATE SOURCE: Inst. Photobiol., Minsk, USSR
SOURCE: Biofizika (1988), 33(6), 1023-8
CODEN: BIOFAI; ISSN: 0006-3029
DOCUMENT TYPE: Journal
LANGUAGE: Russian
AB It was shown by ESR and tryptophan phosphorescence at room temp. that Con A at 10 mg/mL **binds** with glycoprotein **receptors** on the surface of salivary gland cells of **Drosophila** virilis larva beyond gap junction regions initiating generalized structural reorganization of plasma membranes. The reorganization is **coupled** with a decrease in permeability of intercellular channels to small inorg. ions and fluorescein. Treatment of cells with dimethylsuberimidate-HCl, a reagent producing intra- and interprotein links which stabilize the network of plasma membranes, blocked the capacity of Con A to initiate structural reorganization of the membranes and disrupt intercellular communications. Con A-induced structural and functional effects were abolished by addn. of 4 mM .alpha.-D-glucopyranoside, which displaced the lectin on the cell surface **receptors**. The obtained results suggest the existence of a structural membrane mechanism of distal regulation of intercellular communications according to the following pattern: local structural reorganizations initiated beyond gap junction regions, generalization of the structural reorganization over the protein network of plasma membranes, involvement of high-permeability contact membranes in the reorganization, change in the structural organization and

joining of protein half-channels of gap junctions, and modification of intercellular channel permeability of small inorg. ions and low-mol.-wt. org. compds.

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